```
EZH2 ── 1   MGQTGKKSEKGPVCWRKRVKSEYMRLRQLKRFRRADEVKSMFSSNRQKIL   50
                .|.|.|. |::|||||:::|| ||::|||||:|. : .|::.
E(z)  ── 1   .....MNSTKVPPEWKRRVKSEYIKIRQQKRYKRADEIKEAWIRNWDEHN   45

       51   ERTEILNQEWKQRRIQPVHILTSVSSLRGTRECSVTSDLDFP..TQVIPL   98
                ...: | |.|.:. .|.  .. : .::. ..||| ::| .| :|:
       46   HNVQDLYCESKVWQAKPYD....PPHVDCVKRAEVTSYNGIPSGPQKVPI   91

       99   KTLNAVASVPIMYSWSPLQQNFMVEDETVLHNIPYMGDEVLDQDGTFIEE   148
                .:|||..:|.||.|.| |||||||||||||||||||||||||.||.||||
       92   CVINAVTPIPTMYTWAPTQQNFMVEDETVLHNIPYMGDEVLDKDGKFIEE   141

      149   LIKNYDGKVHCDRECGFINDEIFVELVNAL...................   178
                ||||||||||||::::|::|.||||||:||
      142   LIKNYDGKVHCDKDPSFMDDAIFVELVHALMRSYSKELEEAAPSTSTAIK   191

      179   .......GQYNDDDDDDDGDDPE.....EREEKQKDLED..........H   206
                | :||: | :.|.|  |:.|.. ||.|
      192   TEPLAKSKQGEDDGVVDVDADCESPMKLEKTESKGDLTDVEKKETEEPVE   241

      207   RDDKESRPPRK.......FPSDKIFEAISSMFPDKGTAEELKEKYKELTE   249
                :| : :|:.    ||. ||:|||. ||||||||:|||| ||||
      242   TEDADVKPAVEEVKDKLPFPAPIIFQAISANFPDKGTAQELKEKYIELTE   291

      250   QQLPGALPPECTPNIDGPNAKSVQREQSLHSFHTLFCRRCFKYDCFLHPF   299
                :| | |: |.|||||||. .|.|| ||..:|||||||||||||||||.:
      292   HQDPER.PQECTPNIDGIKAESVSRERTMHSFHTLFCRRCFKYDCFLHRL   340

      300   ..HATPNTYKRKNTETALDNKRCGPQCYQHLEGAKEFAAALTAERIKTPP   347
                ||.|| ||:.| ..||: || ::| || || ||||
      341   QGHAGPNLQKRRYPELKPFAEPCSNSCYMLIDGMKEKLAA....DSKTPP   386

      348   KRPGGRRRGRLPNNSSRPSTPTINVLESKDTDSDREAGTETGGENNDKEE   397
                : ..:.:|: ..:.:. .|.| :.
      387   ......................IDSCNEASSEDSNDSNSQFSNKDFNH   412

      398   EEKKDET.SSSSEANSRCQTPIKMKPNIEPPENVEWSGAEASMFRVLIGT   446
                |:.||:. .|.| .... : ||...: | |.||:..::|||   .
      413   ENSKDNGLTVNSAAVAEINSIMAGMMNITSTQCV.WTGADQALYRVLHKV   461

      447   YYDNRCAIARLIGTKTCRQVYEFRVKESSIIAPAPAEDVDTPPRKKKRKH   496
                |..|:|||: : |||||||||| ||.:. .. :  ||||||:.||
      462   YLKNYCAIAHNMLTKTCRQVYEFAQKEDAEFSFEDLRQDFTPPRKKKKKQ   511
```

GTP   chromo   SET

Su(var)3–9

SUV39H   43%

635

412
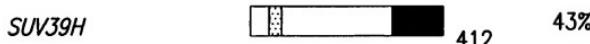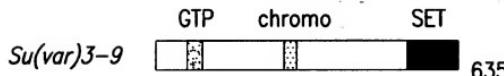
FIG. 2A

```
SUV39H
   └─ 1   MAENLKGCSVCCKSSWNQLQDLCRLAKLSCPALGISKRNLYDEEVEYLCD   50  ┐
Su(var)3-9                    :.:||...:          ::||:.             │
   └─ 207  ...................MGVIAKRPPKG........EYVVERIEC  226  │ CHROMO
                                                                   │  39%
      51   YKKIREQEYYLVKWRGYPDSESTWEPRQNLK..................   81  │
              ..|:::|||||.||||.|||..|.|                          │
      227  VENDQYQPVFFVKWLGYHDSENTWESLANVADCAEMEKFVERHQQLYETY  276  ┘

      82   CVRILKQFHKDLERELLRRHHRSKTPRHLDP.SLANYLVQKAKQRRALRR  130
              ..:|.:::.|:||  |.:    .. .:|.|. |: |.|||.|
      277  IAKITTELEKQLEALPLMENITVAEVDAYEPLNLQIDLILLAQYRAACSR  326

      131  WEQE..........LNAKRSHLGR.....................IT  146
              .:.|            :.||.::.|                      |
      327  SQREPQKIGERALKSMQIKRAQFVRRKQLADLALFEKRMNHVEKPSPPIR  376

      147  VENEVDLDGPPRAFVYINEYRVGEGITLNQVA.VGCECQDCLWAPTGQCC  195
              |||::|||. ...|:||:: ::|.::.  :.: |||.|   ..|:.
      377  VENNIDLDTIDSNFMYIHDNIIGKDVPKPEAGIVGCKCTEDTEECTASTK  426

      196  PGASL..HKFAYNDQG.QVRLRAGLPIYECNSRCRCGYDCPNRVVQKGIR  242
              ..|.:  .|||:  . .:|||:| :|||||||.|: .|.||:||.|.
      427  CCARFAGELFAYERSTRRLRLRPGSAIYECNSRCSCDSSCSNRLVQHGRQ  476

      243  YDLCIFRTDDGRGWGVRTLEKIRKNSEVMEYVGEIITSEEAERRGQIYDR  292  ┐
              .|.:|:|.:|.||||. .:||.||.||::||||||. :|.|          │
      477  VPLVLFKTANGSGWGVRAATALRKGEEVCEYIEEIITSDEANERGRAYDD  526  │
                                                                   │
      293  QGATYLFDLDY...VEDVYIVDAAYYGNISHFVNHSCDPNLQVYNVEIDN  339  │
              .|.||||||||    :.  ||:||| ||||||.:||||||||.|: .:|:.  │
      527  NGRTYLFDLDYNTAQDSEYTIDAAYYGNISHFINHSCDPNLAVEPCWIEH  576  │ SET
                                                                   │ 51%
      340  LDERLPRIAFFATRTIRAGEELTFDYNMQVDPVDMESTRMDSNFGLAGLP  389  │
              |. ||::.||. |:|:|||||.|||:..| |: ...:...            │
      577  LNVALPHLVFFTLRPIKAGEELSFDY.IRADNEDVPYENLSTA.......  618  │
                                                                   │
      390  GSPKKRVRIECKCGTESCRKYLF                              412  │
              ||:||:|| :.||| ||                                   │
      619  ......VRVECRCGRDNCRKVLF                              635  ┘
```

FIG. 2B

```
E(z)     SDIAGWGIFL KEGAQKNEFI SEYCGEIISQ DEADRRGKVY DK..YMCSFL    50
EZH2     SDVAGWGIFI KDPVQKNEFI SEYCGEIISQ DEADRRGKVY DK..YMCSFL

HRX      SPIHGRGLFC KRNIDAGEMV IEYAGNVIRS IQTDKREKYV DSKGIG.CYM
trx      SHIHGRGLYC TKDIEAGEMV IEYAGELIRS TLTDKRERYV DSRGIG.CYM
C26      SRIHGWGLYA MESIAPDEMI VEYIGQTIRS LVAEEREKAY ERRGIGSSYL
YHR      SAIHNWGLYA LDSIAAKEMI IEYVGERTRQ PVAENMREKRY LKNGIGSSYL

Su3-9    ANGSGWGVRA ATALRKGEFV CEYIEEIITS DEANERGKAY DDNG..RTYL
SUV39H   DDGRGWGVRT LEKIRKNSFV MEYVGEIITS EEAERRGQIY DRQG..ATYL
G9α      TAKMCWGVRA LQTIPQGTFI CEYVGELISD AEAD...V.. .RED..DSYL
KG-1     TQNKCWGIRC LDDIAKGSFV CIYAGKILTD DFADKEGL.. .EMG..DEYF


E(z)     FNLN...... NDFVVDATRK GNKIRFANHS INPNCYAKVM MVTGDH....   100
EZH2     FNLN...... NDFVVDATRK GNKIRFANHS VNPNCYAKVM MVNGDH....

HRX      FRID...... DSEVVDATMH GNRARFINHS CEPNCYSRVI NIDGQK....
trx      FKID...... DNLVVDATMR GNAARFINHC CEPNCYSKVV DILGHK....
C26      FRID...... LHHVIDATKR GNFARFINHC CQPNCYAKVL TIEGEK....
YHR      FRVD...... ENTVIDATKK GGIARFINHC CDPNCTAKII KVGGRR....

Su3-9    FDLDYNTAQD SEYTIDAANY GNISHFINHS CDPNLAVFPC WIEHLNVALP
SUV39H   FDLDY...VE DVYTVDAAYY GNISHFVNHS CDPNLQVYNV FIDNLDERLP
G9α      FDLDNK..DG EVYCIDARYY GNISRFINHL CDPNIIPVRV FMLHQDLRFP
KG-1     ANLDHI..ES VEYIIDAKLE GNLGRYLNHS CSPNLFVQNV FVDTHDLRFP
                 ↓

E(z)     RIGIFAKRAI QPGEELFFDY ..RYGPTEQL K.....FVGI EREMEIV*    150
EZH2     RIGIFAKRAI QTGEELFFDY ..RYSQADAL K.....YVGI EREMEIP*

HRX      HIVIFAMRKI YRGEELTYDY ..KFPIE.DA SNKLPCNCGA KKCRKFLN*
trx      HIIIFAVRRI VGGEELTYDY ..KFPFE.D. .EKIPCSOGS KRCRKYLN*
C26      RIVIYSRTI KKGEEITYDY ..KFPIE... DDKIDCLCGA KTCRGYLN*
YHR      RIVIYALRDI AASEELTYDY ..KFEREKDD EERLPCLCGA PNCKGFLN*

Su3-9    HLVFFTLRPI KAGEELSFDY .IRADNEDVP YENLSTA... ..........
SUV39H   RIAFFATRTI RAGEELTFDY NMQVDPVDME STRMDSNFGL AGLPGSPKKR
G9α      RIAFFSSRDT RTGEELGFDY GDRFW..DIK SKYFTCQCGS EKCKHSAEAI
KG-1     WMAFFASKRI RAGTELTWDY NYEVG..SVE GKELLCCCGA IECR......


E(z)
EZH2

HRX
trx
C26
YHR

Su3-9    VRVECRCGRD NCRKVLF*
SUV39H   VRIECKCCGTE SCRKYLF*
G9α      ALEQSRLARL DPHPELLPEL GSLPPVNT*
KG-1     ....GRLL*
```

FIG.5

EZH2 length: 2600bp (coding: 90-2330)

```
   1  AGGCAGTGGAGCCCCGGCCGCGGCGGCGGCGGCGGCCGCGCGGGGGCGACGCGCGGGAACAACG   60

  61  CGAGTCGGCGCGCGGGACGAAGAATAATCATGGGCCAGACTGGGAAGAAATCTGAGAAGG  120
                                   M  G  Q  T  G  K  K  S  E  K  G

 121  GACCAGTTTGTTGGCGGAAGCGTGTAAAATCAGAGTACATGCGACTGAGACAGCTCAAGA  180
        P  V  C  W  R  K  R  V  K  S  E  Y  M  R  L  R  Q  L  K  R

 181  GGTTCAGACGAGCTGATGAAGTAAAGAGTATGTTTAGTTCCAATCGTCAGAAAATTTTGG  240
        F  R  R  A  D  E  V  K  S  M  F  S  S  N  R  Q  K  I  L  E

 241  AAAGAACGGAAATCTTAAACCAAGAATGGAAACAGCGAAGGATACAGCCTGTGCACATCC  300
        R  T  E  I  L  N  Q  E  W  K  Q  R  R  I  Q  P  V  H  I  L

 301  TGACTTCTGTGAGCTCATTGCGCGGGACTAGGGAGTGTGTCGGTGACCAGTGACTTGGATT  360
        T  S  V  S  S  L  R  G  T  R  E  C  S  V  T  S  D  L  D  F

 361  TTCCAACACAAGTCATCCCATTAAAGACTCTGAATGCAGTTGCTTCAGTACCCATAATGT  420
        P  T  Q  V  I  P  L  K  T  L  N  A  V  A  S  V  P  I  M  Y

 421  ATTCTTGGTCTCCCCTACAGCAGAATTTTATGGTGGAAGATGAAACTGTTTTACATAACA  480
        S  W  S  P  L  Q  Q  N  F  M  V  E  D  E  T  V  L  H  N  I

 481  TTCCTTATATGGGAGATGAAGTTTTAGATCAGGATGGTACTTTCATTGAAGAACTAATAA  540
        P  Y  M  G  D  E  V  L  D  Q  D  G  T  F  I  E  E  L  I  K

 541  AAAATTATGATGGGAAAGTACACGGGGATAGAGAATGTGGGTTTATAAATGATGAAATTT  600
        N  Y  D  G  K  V  H  G  D  R  E  C  G  F  I  N  D  E  I  F

 601  TTGTGGAGTTGGTGAATGCCCTTGGTCAATATAATGATGATGACGATGATGATGATGGAG  660
        V  E  L  V  N  A  L  G  Q  Y  N  D  D  D  D  D  D  D  G  D

 661  ACGATCCTGAAGAAAGAGAAGAAAAGCAGAAAGATCTGGAGGATCACCGAGATGATAAAG  720
        D  P  E  E  R  E  E  K  Q  K  D  L  E  D  H  R  D  D  K  E

 721  AAAGCCGCCCACCTCGGAAATTTCCTTCTGATAAAAATTTTTGAAGCCATTTCCTCAATGT  780
        S  R  P  P  R  K  F  P  S  D  K  I  F  E  A  I  S  S  M  F

 781  TTCCAGATAAGGGCACAGCAGAAGAACTAAAGGAAAAATATAAAGAACTCACCGAACAGC  840
        P  D  K  G  T  A  E  E  L  K  E  K  Y  K  E  L  T  E  Q  Q

 841  AGCTCCCAGGCGCACTTCCTCCTGAATGTACCCCCAACATAGATGGACCAAATGCTAAAT  900
        L  P  G  A  L  P  P  E  C  T  P  N  I  D  G  P  N  A  K  S

 901  CTGTTCAGAGAGAGCAAAGCTTACACTCCTTTCATACGCTTTTCTGTAGGCGATGTTTTA  960
        V  Q  R  E  Q  S  L  H  S  F  H  T  L  F  C  R  R  C  F  K

 961  AATATGACTGCTTCCTACATCCTTTTCATGCAACACCCAACACTTATAAGCGGAAGAACA 1020
        Y  D  C  F  L  H  P  F  H  A  T  P  N  T  Y  K  R  K  N  T

1021  CAGAAACAGCTCTAGACAACAAACCTTGTGGACCACAGTGTTACCAGCATTTGGAGGGAG 1080
        E  T  A  L  D  N  K  P  C  G  P  Q  C  Y  Q  H  L  E  G  A

1081  CAAAGGAGTTTGCTGCTGCTCTCACCGCTGAGCGGATAAAGACCCCACCAAAACGTCCAG 1140
        K  E  F  A  A  A  L  T  A  E  R  I  K  T  P  P  K  R  P  G
```

FIG. 6A

```
1141  GAGGCCGCAGAAGAGGACGGCTTCCCAATAACAGTAGCAGGCCCAGCACCCCCACCATTA  1200
        G  R  R  R  G  R  L  P  N  N  S  S  R  P  S  T  P  T  I  N

1201  ATGTGCTGGAATCAAAGGATACAGACAGTGATAGGGAAGCAGGGACTGAAACGGGGGGAG  1260
        V  L  E  S  K  D  T  D  S  D  R  E  A  G  T  E  T  G  G  E

1261  AGAACAATGATAAAGAAGAAGAAGAGAAGAAAGATGAAACTTCGAGCTCCTCTGAAGCAA  1320
        N  N  D  K  E  E  E  E  K  K  D  E  T  S  S  S  S  E  A  N

1321  ATTCTCGGTGTCAAACACCAATAAAGATGAAGCCAAATATTGAACCTCCTGAGAATGTGG  1380
        S  R  C  Q  T  P  I  K  M  K  P  N  I  E  P  P  E  N  V  E

1381  AGTGGAGTGGTGCTGAAGCCTCAATGTTTAGAGTCCTCATTGGCACTTACTATGACAATT  1440
        W  S  G  A  E  A  S  M  F  R  V  L  I  G  T  Y  Y  D  N  F

1441  TCTGTGCCATTGCTAGGTTAATTGGGACCAAAACATGTAGACAGGTGTATGAGTTTAGAG  1500
        C  A  I  A  R  L  I  G  T  K  T  C  R  Q  V  Y  E  F  R  V

1501  TCAAAGAATCTAGCATCATAGCTCCAGCTCCCGCTGAGGATGTGGATACTCCTCCAAGGA  1560
        K  E  S  S  I  I  A  P  A  P  A  E  D  V  D  T  P  P  R  K

1561  AAAAGAAGAGGAAACACCGGTTGTGGGCTGCACACTGCAGAAAGATACAGCTGAAAAAGG  1620
        K  K  R  K  H  R  L  W  A  A  H  C  R  K  I  Q  L  K  K  D

1621  ACGGCTCCTCTAACCATGTTTACAACTATCAACCCTGTGATCATCCACGGCAGCCTTGTG  1680
        G  S  S  N  H  V  Y  N  Y  Q  P  C  D  H  P  R  Q  P  C  D

1681  ACAGTTCGTGCCCTTGTGTGATAGCACAAAATTTTTGTGAAAAGTTTTGTCAATGTAGTT  1740
        S  S  C  P  C  V  I  A  Q  N  F  C  E  K  F  C  Q  C  S  S

1741  CAGAGTGTCAAAACCGCTTTCCGGGATGCCGCTGCAAAGCACAGTGCAACACCAAGCAGT  1800
        E  C  Q  N  R  F  P  G  C  R  C  K  A  Q  C  N  T  K  Q  C

1801  GCCCGTGCTACCTGGCTGTCCGAGAGTGTGACCCTGACCTCTGTCTTACTTGTGGAGCCG  1860
        P  C  Y  L  A  V  R  E  C  D  P  D  L  C  L  T  C  G  A  A

1861  CTGACCATTGGGACAGTAAAAATGTGTCCTGCAAGAACTGCAGTATTCAGCGGGGCTCCA  1920
        D  H  W  D  S  K  N  V  S  C  K  N  C  S  I  Q  R  G  S  K

1921  AAAAGCATCTATTGCTGGCACCATCTGACGTGGCAGGCTGGGGGATTTTTATCAAAGATC  1980
        K  H  L  L  L  A  P  S  D  V  A  G  W  G  I  F  I  K  D  P

1981  CTGTGCAGAAAAATGAATTCATCTCAGAATACTGTGGAGACATTATTTCTCAAGATGAAG  2040
        V  Q  K  N  E  F  I  S  E  Y  C  G  E  I  I  S  Q  D  E  A

2041  CTGACAGAAGAGGGAAAGTGTATGATAAATACATGTGCAGCTTTCTGTTCAACTTGAACA  2100
        D  R  R  G  K  V  Y  D  K  Y  M  C  S  F  L  F  N  L  N  N

2101  ATGATTTTGTGGTGGATGCAACCCGCAAGGGTAACAAAATTCGTTTTGCAAATCATTCGG  2160
        D  F  V  V  D  A  T  R  K  G  N  K  I  R  F  A  N  H  S  V

2161  TAAATCCAAACTGCTATGCAAAAGTTATGATGGTTAACGGTGATCACAGGATAGGTATTT  2220
        N  P  N  C  Y  A  K  V  M  M  V  N  G  D  H  R  I  G  I  F

2221  TTGCCAAGAGAGCCATCCAGACTGGCGAAGAGCTGTTTTTTGATTACAGATACAGCCAGG  2280
        A  K  R  A  I  Q  T  G  E  E  L  F  F  D  Y  R  Y  S  Q  A
```

FIG. 6B

SUV39H length: 2732bp (coding: 45-1284)

```
  1  TCGCGAGGCCGGCTAGGCCCGAATGTCGTTAGCCGTGGGGAAAGATGGCCGGAAAATTTAA   60
                                               M  A  E  N  L  K

 61  AAGGCTGCAGCGTGTGTTGCAAGTCTTCTTGGAATCAGCTGCAGGACCTGTGCCGCCTGG  120
      G  C  S  V  C  C  K  S  S  W  N  Q  L  Q  D  L  C  R  L  A

121  CCAAGCTCTCCTGCCCTGCCCTCGGTATCTCTAAGAGGAACCTCTATGACTTTGAAGTCG  180
      K  L  S  C  P  A  L  G  I  S  K  R  N  L  Y  D  F  E  V

181  AGTACCTGTGCCGATTACAAGAAGATCCGCGAACACGAATATTACCTGGTGAAATGGCGTG  240
      Y  L  C  D  Y  K  K  I  R  E  Q  E  Y  Y  L  V  K  W  R  G

241  GATATCCAGACTCAGAGAGCACCTGGGAGCCACGGCAGAATCTCAAGTGTGTGCGTATCC  300
      Y  P  D  S  E  S  T  W  E  P  R  Q  N  L  K  C  V  R  I  L

301  TCAAGCAGTTCCACAAGGACTTAGAAAGGGAGCTGCTCCGGCGGCCACCACCGGTCAAAGA  360
      K  Q  F  H  K  D  L  E  R  E  L  L  R  R  H  H  R  S  K  T

361  CCCCCCGGCACCTGGACCCAAGCTTGGCCAACTACCTGGTGCAGAAGGCCAAGCAGAGGC  420
      P  R  H  L  D  P  S  L  A  N  Y  L  V  Q  K  A  K  Q  R  R

421  GGGCGCTCCGTCGCTGGGAGCAGGAGCTCAATGCCAAGCGCAGCCATCTGGGACGCATCA  480
      A  L  R  R  W  E  Q  E  L  N  A  K  R  S  H  L  G  R  I  T

481  CTGTAGAGAATGAGGTGGACCTGGACGGCCCTCCCGGGGCCTTCGTGTACATCAATGAGT  540
      V  E  N  E  V  D  L  D  G  P  P  R  A  F  V  Y  I  N  E  Y

541  ACCGTGTTGGTGAGGGCATCACCCTCAACCAGGTGGCTGTGGGCTGCGAGTGCCAGGACT  600
      R  V  G  E  G  I  T  L  N  Q  V  A  V  G  C  E  C  Q  D  C

601  GTCTGTGGGCACCCACTGGAGGCTGCTGCCCGGGGGCGTCACTGCACAAGTTTGCCTACA  660
      L  W  A  P  T  G  G  C  C  P  G  A  S  L  H  K  F  A  Y  N

661  ATGACCAGGGCCAGGTGCGGCTTCGAGCCGGGCTGCCCATCTACGAGTGCAACTCCCGCT  720
      D  Q  G  Q  V  R  L  R  A  G  L  P  I  Y  E  C  N  S  R  C

721  GCCGCTGCGGCTATGACTGCCCAAATCGTGTGGTACAGAAGGGTATCCGATATGACCTCT  780
      R  C  G  Y  D  C  P  N  R  V  V  Q  K  G  I  R  Y  D  L  C

781  GCATCTTCCGGACGGATGATGGGCGTGGCTGGGGCGTCCGCCACCCTGGAGAAGATTCGCA  840
      I  F  R  T  D  D  G  R  G  W  G  V  R  T  L  E  K  I  R  K

841  AGAACAGCTTCGTCATGGAGTACGTGGGAGAGATCATTACCTCAGAGGAGGCAGAGCGGC  900
      N  S  F  V  M  E  Y  V  G  E  I  I  T  S  E  E  A  E  R  R

901  GGGGCCAGATCTACGACCGTCAGGGCGCCACCTACCTCTTTGACCTGGACTACGTGGAGG  960
      G  Q  I  Y  D  R  Q  G  A  T  Y  L  F  D  L  D  Y  V  E  D

961  ACGTGTACACCGTGGATGCCGCCTACTATGGCAACATCTCCCACTTTGTCAACCACAGTT  1020
      V  Y  T  V  D  A  A  Y  Y  G  N  I  S  H  F  V  N  H  S  C

1021 GTGACCCCAACCTGCAGGTGTACAACGTCTTCATAGACAACCTTGACGAGCGGCTGCCCC  1080
      D  P  N  L  Q  V  Y  N  V  F  I  D  N  L  D  E  R  L  P  R

1081 GCATCGCTTTCTTTGCCACAAGAACCATCCGGGCAGGCGAGGAGCTCACCTTTGATTACA  1140
      I  A  F  F  A  T  R  T  I  R  A  G  E  E  L  T  F  D  Y  N
```

FIG. 7A